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SSISWINESINE

Figure

HSEMMERE RECEPTOR SECTOR ENSPOYOUS

Sequence and pentamer URS distribution

SWOODLR VIK TRUTKITRIASATTEGAWITESIFILWATEPIKGWNHEMOOTSWR R EDK CETDENDV STIVSESVADILEV GAVAVKERNIE

II WIEK II WATANEN EKAR PIJEIN MEMENAKE EKKE AN OROOHR FEETNER SEPISESETKE BEN PENPK IG

DAIKHK PGK FSPMEVIKHR K PK DAGGGSVEKHSPSOTPK FMK SPVATSOEDDR EVDKHLAG

EVHINGA AATESSRID VAVAVINR ISHGOLK IIDHOGINIH GASEIISHD<u>OMEGDSOSHSR TIDSDIFT</u>

GK KR SGSNTGEDYTK FTWK F LR SHSR OKNSGEHMIR ER KRAK OLGENA

EFMVITATIOK NEGNEHEHMETTEWIGENINGENENELIAMPLENENENEK KATERIA

Figure

Figure 3

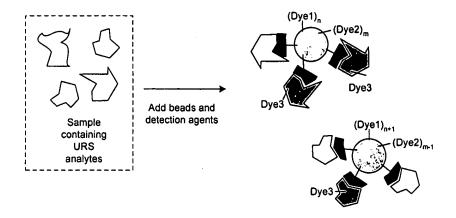


Figure 4

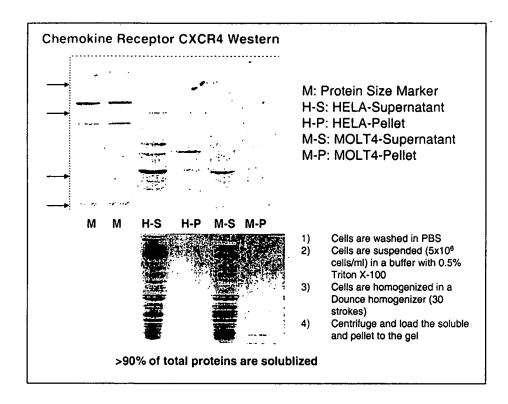
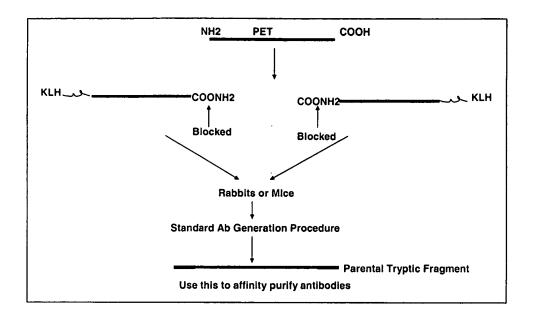


Figure 5



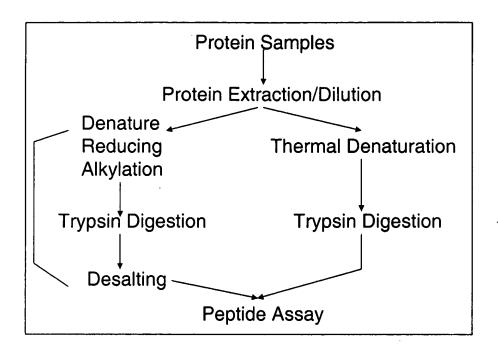


Figure 7

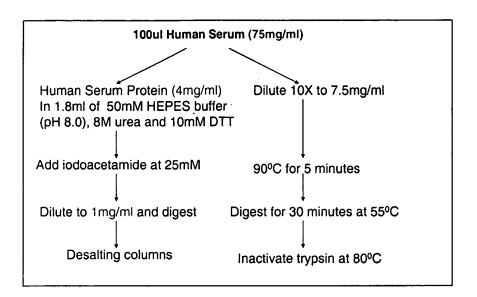


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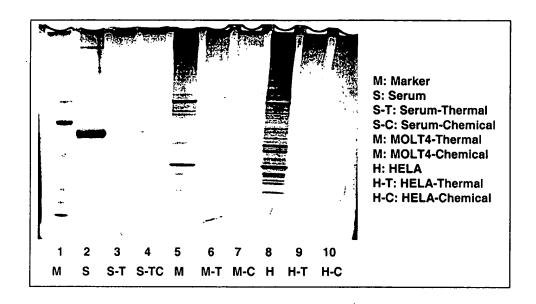
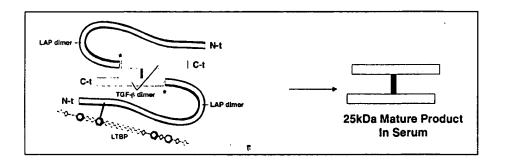


Figure 9



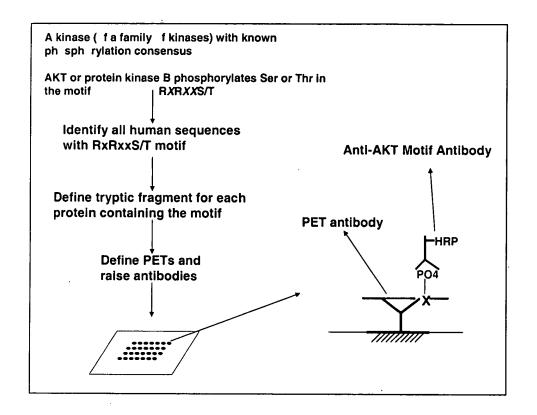


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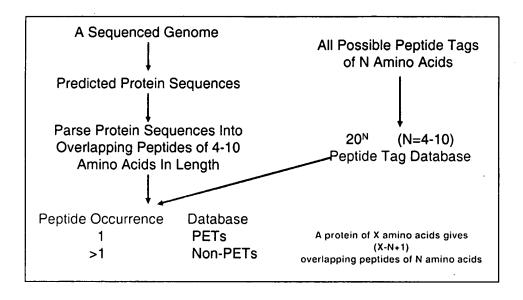


Figure 12

Tag Length (amino acids)	All Possible Tags	Total PETs	Total Non-PETs (non-redundant)
4	160,000	745	158,862
5 6	3.2x10 ⁶ 6.4x10 ⁷	560,309 4,609,172	1,684,684 2,350,532
7	1.28×10 ⁹	6,652,224	1,848,908
8	2.56x10 ¹⁰	7,018,340	1,744,029
9 10	5.12x10 ¹¹ 1.02x10 ¹³	7,138,933	1,714,971 1,695,512
-	tein sequences analyzed 4-10mr peptides	7,216,090 in Total Tag Space in	B Base Found in Human Proteoms 10 5

Figure 13

in of PET (a	imino acids)	Prtins	WITH PEIS	Pr teome Coverage
4		684	4	2.35%
5		23,	446	80.64%
6		26,	069	89.66%
7		26,	184	90.05%
8		26,216		90.16%
9		26,	238	90.24%
10		26,	250	90.28%
Average PET per Tagged Protein	300 250 200 150 100 50			
	PET	Length (amino	9 10 acids)	

Figure 14

PET Length (Amino Acids)		ETs/Tagged Protein e Trypsin Cleavage
5	24	16
6	177	98
8	268	129
¹⁰ }		0000 (
00 _	Le u	os
0 X= ~49	# 15 mm	0000 X=~8.5
	- 10 - 10	0000
	m ber	0000
	E n N	
	1 141 161 181 20	1 11 21 31 41 51 61 71 81 9
Fragment Num	ber .	Fragment Size (amino acids)

Figure 15

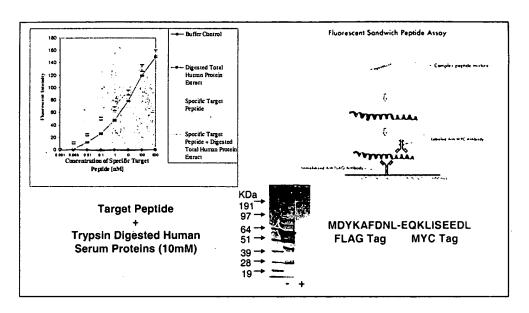


Figure 16

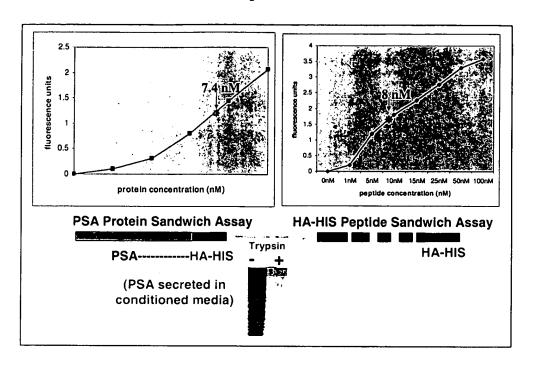


Figure 17

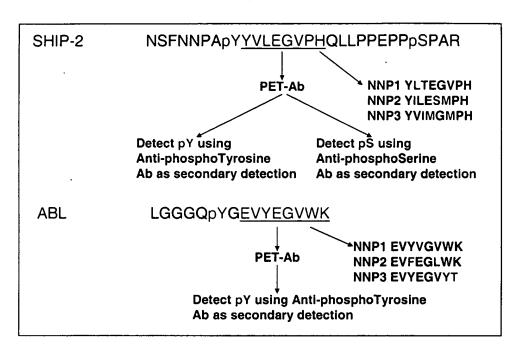
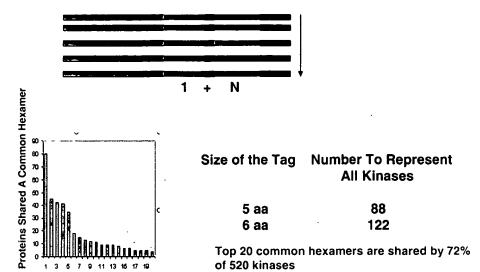


Figure 18



7 9 11 13 15 17 19 Top 20 Common hexamers Top 20 common hexamers are shared by 72% of 520 kinases

Figure 19

Protein	Parental Tryptic Peptide	Also Detect
BRAF	WSGSHQFEQLSGSILWMAPEVIR*	
DLK	MSFAGTVAWMAPEVIR	
GCK	SFIGTPYWMAPEVAAVER	
HH498	WMAPEVFTQCTR	
HPK1	LSFIGTPYWMAPEVAAVALK	
LOK	DSFIGTPYWMAPEVVMCETMK	KSH1,2,HPK1, SLK
LZK	MSFAGTVAWMAPEVIR	
MAP3K	SMHGTPYWMAPEVINESGYGR	
MST1	NTVIGTPFWMAPEVIQEIGYNCVR	MST2 .
MST4	NTFVGTPFWMAPEVIQQSAYDSK	
MYO3 A	NTSVGTPFWMAPEVIACEQQLDTTYDAR	MY03B
муозв	NTSVGTPFWMAPEVIACEQQYDSSYDAR	MY03A
ZC1/HGK	NTFIGTPYWMAPEVIACDENPDATYDYR	ZC2, ZC3
OSR1	TFVGTPCWMAPEVMEQVR	
PAK1	STMVGTPYWMAPEVVTR	PAK2,3
PAK5	SLVGTPYWMAPEVISR	PAK6
RAF1	WSGSQQVEQPTGSVLWMAPEVIR	
STLK3	TFVGTPCWMAPEVMEQVR	
TAO1	ASMASPANSFVGTPYWMAPEVILAMDEGQYDGK	TAO3
TAO2	ASIMAPANSFVGTPYWMAPEVILAMDEGQYDGK	
TESK1	EPLAVVGSPYWMAPEVLR	
ZAK	TTHMSLVGTFPWMAPEVIQSLR	
BLI	JE = PET	
	D = Commone Epitope	

Figure 20

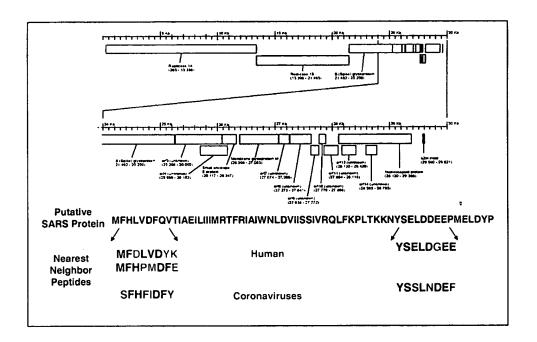


Figure 21

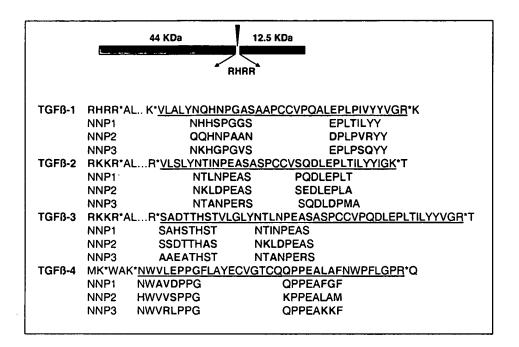


Figure 22

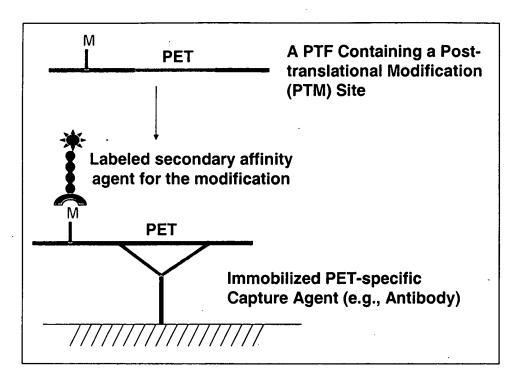


Figure 23

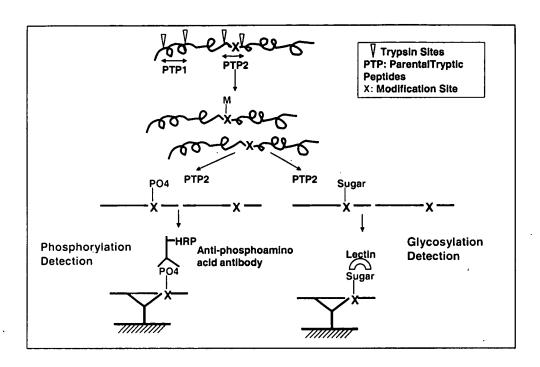


Figure 24

